REMARKS

Applicants have recently identified an obvious mistake in the formal drawing of Figure 3. Specifically, Figure 3 was inadvertently truncated at the C-terminus at position 1065 of the 1100 amino acid protein. This is clearly a typographical error and not new material as the correct protein was disclosed in Figure 16 as TH-1. Moreover, the correct Figure 3 was disclosed in U.S. Application Serial No. 09/969,668, filed on October 25, 2000, of which the instant application is a continuation in part. As such and in compliance with 37 C.F.R. 1.121(d), Applicants enclose herewith for the examiner's approval a proposed revised formal drawing of Figure 3 and a copy of the figure with the requested amendment shown as underlined text. Applicants submit that this amendment is not new matter and request its entry.

The sequence listing is also being corrected to correct this error and to eliminate duplication and overlap in the previously filed copy of the sequence listing of sequences 3 and 4 with sequences 8 and 9 and to include proper reference to the sequences in the corrected sequence listing. Attached hereto is a marked-up version of the changes made to the specification by the current amendment. The attached page is captioned "Version with markings to show changes made."

Entry of this amendment is respectfully requested. The amendments are made in adherence with 37 C.F.R. § 1.821-1.825. This amendment is accompanied by a floppy disk containing the above named corrected sequence, SEQUENCE ID NUMBERS 1-17 in computer readable form, and a paper copy of the corrected sequence information. The computer readable sequence listing was prepared through use of the software program "PatentIn" provided by the PTO. The information contained in the computer readable disk is identical to that of the paper copy. This amendment contains no new matter. Applicant

submits that this amendment, the accompanying computer readable sequence listing, and the paper copy thereof serve to place this application in a condition of adherence to the rules 37 C.F.R. § 1.821-1.825.

Please direct any calls in connection with this application to the undersigned at (415) 781-1989.

Respectfully submitted,

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

IN THE SPECIFICATION:

Paragraph beginning at page 7, line 9, has been amended as follows:

— Figure 16 shows the sequence of TaHo-1 ~~(SEQ ID NO:8)~~ (SEQ ID NO:3) and TaHo-2 ~~(SEQ ID NO:9)~~ (positions 1-338 of SEQ ID NO:4). The figure further identifies the E and F residues that are substituted and the amino acid sequences that are deleted in TaHo protein variants set forth ~~(SEQ ID NOS:10-12)~~ (SEQ ID NOS:8-10). Also indicated are the amino acid sequences comprising ankyrin repeats, the SAM domain, and the PARP domain.—

Paragraph beginning at page 12, line 16, has been amended as follows:

— In a preferred embodiment, dominant negative TaHo protein isoforms are provided. Included and preferred among such TaHo proteins are proteins having mutations in an NAD+ binding site. More preferred among these proteins are those with F→L, or E→A, or F→L and E→A mutations in an NAD+ binding site, as those depicted in Figures 5 and 16 ~~(SEQ ID NOS:10-12)~~ (SEQ ID NOS:8-10). Also preferred are TaHo proteins with deletions in the PARP domain at the C-terminus, preferably from amino acids 961-976, or amino acids 430-476, as set forth in Figure 16. Also highly preferred is a TaHo protein with such a C-terminus deletion from amino acids 961-976 as set forth in Figure 16, and having an E→A mutation or an F→L mutation or F→L and E→A mutations.—

Paragraph beginning at page 39, line 6, has been amended as follows:

— Particularly preferred among such dominant negative cell cycle proteins are dominant negative TaHo proteins having mutations in an NAD+ binding site. More preferred among these proteins are those with F→L, E→A, or F→L and E→A amino acid substitutions in an NAD+ binding site, as those depicted in Figure 5. Also preferred are TaHo proteins

with deletions in the PARP domain, preferably from amino acids 461-476 or 430-476 as depicted in Figure 16 ~~(SEQ ID NOS:10-12)~~ (SEQ ID NOS:8-10). Also preferred is a TaHo protein with such a C-terminus deletion from amino acids 461-476 as set forth in Figure 16 and having an F→L, E→A, or F→L and E→A amino acid substitution in an NAD+ binding site, as depicted in Figure 16.—

Paragraph beginning at page 44, line 36, has been amended as follows:

— A number of cyclin destruction boxes are known in the art, for example, cyclin A has a destruction box comprising the sequence RTVLGVIGD ~~(SEQ ID NO:13)~~ (SEQ ID NO:11); the destruction box of cyclin B1 comprises the sequence RTALGDIGN ~~(SEQ ID NO:14)~~ (SEQ ID NO:12). See Glotzer et al., Nature 349:132-138 (1991). Other destruction boxes are known as well: YMTVSIIDRFMQDSCVPKKMLQLVGVT (rat cyclin B; ~~SEQ ID NO:15~~ SEQ ID NO:13); KFRLLQETMYMTVSIIDRFMQNSCVPKK (mouse cyclin B; ~~SEQ ID NO:16~~ SEQ ID NO:14); RAILIDWLIQVQMKFRLLQETMYMTVS (mouse cyclin B1; ~~SEQ ID NO:17~~ SEQ ID NO:15); DRFLQAQLVCRKKLQVVGITALLLASK (mouse cyclin B2; ~~SEQ ID NO:18~~ SEQ ID NO:16); and MSVLRGKLQLVGTAAMLL (mouse cyclin A2; ~~SEQ ID NO:19~~ SEQ ID NO:17).–

On page 63, immediately preceding the heading "CLAIMS," the previously submitted sequence listing was deleted and the enclosed text entitled "Sequence Listing" was inserted into the specification.

In the Figures:

Figure 3 was replaced with the enclosed replacement formal drawing for Figure 3.